

Amendments to the claims

In the claims:

Claims 1-91(Canceled)

92. (Currently Amended) A method of predicting for the hepatotoxicity of a test compound, comprising:

(a) preparing a gene expression profile of at least ten genes from a liver tissue or liver cell sample exposed to the test compound; and

(b) comparing the expression levels of said at least ten genes from the gene expression profile to a database comprising the gene expression levels of said at least ten genes derived from liver tissue or liver cell samples that have been exposed to at least one known hepatotoxin, wherein said at least ten genes are selected from the genes and ESTs sequences listed in any one of Tables 3A-3S, thereby predicting for the hepatotoxicity of the test compound.

93. (Currently Amended) [A] The method of claim 92, wherein the gene expression profile prepared from the liver tissue or liver cell sample comprises the level of expression for at least 100 genes.

94. (Currently Amended) [A] The method of claim 92, wherein expression levels for said at least ten genes from the gene expression profile are compared to Toxic Mean and/or NonToxic Mean values in a database comprising any one of Tables 3A-3S.

95. (Currently Amended) [A] The method of claim 94, wherein the level of expression for each gene is normalized prior to comparison.

96. (Currently Amended) [A] The method of claim 92, wherein the database comprises all of the data in any one of Tables 3A-3S.

97. (Previously Presented) The method of claim 92, wherein the expression levels of at least 15 genes are compared to the database.

98. (Previously Presented) The method of claim 92, wherein the expression levels of at least 20 genes are compared to the database.

99. (Previously Presented) The method of claim 92, wherein the expression levels of at least 25 genes are compared to the database.

100. (Previously Presented) The method of claim 92, wherein the expression levels of at least 30 genes are compared to the database.

101. (Previously Presented) The method of claim 92, wherein the expression levels of at least 50 genes are compared to the database.

102. (Previously Presented) The method of claim 92 wherein the expression levels of at least 75 genes are compared to the database.

103. (Previously Presented) The method of claim 92, wherein the expression levels of at least 100 genes are compared to the database.

104. (Previously Presented) The method of claim 92, wherein the liver cell or liver tissue sample is exposed to the test compound *in vivo* and the liver cell or liver tissue samples from which database information is derived are exposed to the at least one known hepatotoxin *in vivo*.

105. (Currently Amended) [A] The method of claim 104, wherein the hepatotoxicity is associated with at least one liver disease pathology selected from the group consisting of liver damage induced by hepatitis, liver damage induced by NSAIDS, liver necrosis with fatty liver, liver necrosis without fatty liver and liver damage induced by compounds that form protein adducts.

106. (Currently Amended) [A] The method of claim 92, wherein the hepatotoxin is selected from the group consisting of amitryptiline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-

14643.

107. (Currently Amended) [A] The method of claim 92, wherein the gene expression profile is produced by hybridization of nucleic acids to a microarray.

108. (Currently Amended) [A] The method of claim 92, wherein the liver cell or liver tissue sample is a rat liver cell or rat liver tissue sample.

109. (Currently Amended) [A] The method of claim 92, wherein said selected genes are rat genes.

110. (Currently Amended) [A] The method of claim 104, wherein the hepatotoxicity is liver necrosis.

111. (Currently Amended) A method of predicting for the liver toxicity of a test compound, comprising:

(a) preparing a gene expression profile of at least ten genes from a liver tissue or liver cell sample exposed to the test compound; and

(b) comparing the expression levels of said ~~at least ten~~ genes from the gene expression profile to a database comprising the gene expression levels of said ~~at least ten~~ genes derived from liver tissue or liver cell samples that have been exposed to at least one known liver toxin, wherein said at least ten genes are selected from the genes and ESTs sequences listed in any one of Tables 3A-3S, thereby predicting for the liver toxicity of the test compound.

112. (Currently Amended) [A] The method of claim 111, wherein the gene expression profile prepared from the liver tissue or liver cell sample comprises the level of expression for at least 100 genes.

113. (Currently Amended) [A] The method of claim 111, wherein expression levels for said at least ten genes from the gene expression profile are compared to Toxic Mean and/or NonToxic Mean values in a database comprising Tables 3A-3S.

114. (Currently Amended) [A] The method of claim 111, wherein the level of expression for each gene is normalized prior to comparison.

115. (Currently Amended) [A] The method of claim 111, wherein the database comprises all of the data in any one of Tables 3A-3S.

116. (Previously Presented) The method of claim 111, wherein the expression levels of at least 15 genes are compared to the database.

117. (Previously Presented) The method of claim 111, wherein the expression levels of at least 20 genes are compared to the database.

118. (Previously Presented) The method of claim 111, wherein the expression levels of at least 25 genes are compared to the database.

119. (Previously Presented) The method of claim 111, wherein the expression levels of at least 30 genes are compared to the database.

120. (Previously Presented) The method of claim 111, wherein the expression levels of at least 50 genes are compared to the database.

121. (Previously Presented) The method of claim 111, wherein the expression levels of at least 75 genes are compared to the database.

122. (Previously Presented) The method of claim 111, wherein the expression levels of at least 100 genes are compared to the database.

123. (Previously Presented) The method of claim 111 wherein the liver cell or liver tissue sample is exposed to the compound *in vivo* and the liver cell or liver tissue samples from which database information is derived are exposed to the at least one known liver toxin *in vivo*.

124. (Currently Amended) [A] The method of claim 123, wherein the liver toxicity is associated with at least one liver disease pathology selected from the group consisting of liver damage induced by hepatitis, liver damage induced by NSAIDS, liver necrosis with fatty liver, liver necrosis without fatty liver and liver damage induced by compounds that form protein adducts.

125. (Currently Amended) [A] The method of claim 123, wherein the liver toxin is selected from the group consisting of amitryptiline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-14643.

126. (Currently Amended) [A] The method of claim 111, wherein the gene expression profile is produced by hybridization of nucleic acids to a microarray.

127. (Currently Amended) [A] The method of claim 111, wherein the liver cell or liver tissue sample is a rat liver cell or rat liver tissue sample.

128. (Currently Amended) [A] The method of claim 111, wherein said selected genes are rat genes.

129. (Currently Amended) [A] The method of claim 123 wherein the liver toxicity is liver necrosis.